Transcriptional search to identify and assess reference genes for expression analysis in *Solanum lycopersicum* L. under stress and hormone treatments

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**Background**
Tomato (*Solanum lycopersicum*) is a model plant for research on fruit development and stress response, in which gene expression analysis is a frequently conducted. Quantitative polymerase chain reaction (qPCR) is a widely used technique for gene expression analysis, and the selection of reference genes may affect the accuracy of results and even conclusions. Although there have been some frequently used reference genes in tomato, it has been shown that the expressions of these genes are not constant in different tissues and environmental conditions. Moreover, no genomic identification of reference gene was performed in tomato.

**Methods**
In this study, we mined the publicly available transcriptional sequencing data and screened out some candidate reference genes. The expression stability of the candidate reference genes and several traditional ones were evaluated experimentally.

**Results** (up to 4 figures and tables can be included)

![Figure 1](image_url) KEGG pathway enrichment analysis of the candidate reference genes from RNA-seq
Fifteen novel candidate reference genes were screened out from public transcriptional sequencing data, and most of them were housekeeping genes in plant cells. The expression stability of the novel candidate reference genes together with seven traditionally used ones in previous research were evaluated when the tomato seedlings were treated with various stresses and hormones. The results showed that the most stable gene varied under different treatments, and the selected novel reference genes were mostly expressed more stably than the traditionally used ones.

**Conclusion**
Our study suggests that excavating stably expressed genes from transcriptome sequencing data is a reliable approach to screen reference genes. This study provides some stable reference genes for use in future research in tomato roots and leaves under different environmental stimuli.

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**References** (No more than 15 references)